

## SEQUENCE LISTING

<110> DNAVEC RESEARCH INC.

<120> Methods for enhancing exogenous epitope display on MHC class  
through inhibition of TAP activity

<130> D3-A0102P

<140>

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<150> JP 2002-288394

<151> 2002-10-01

<160> 54

<170> PatentIn Ver. 2.0

<210> 1

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 1

Gly Gly Gly Ser

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<210> 2

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 2

Gly Gly Gly Gly Ser

1

5

&lt;210&gt; 3

&lt;211&gt; 10

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: artificially  
synthesized sequence

&lt;400&gt; 3

Gly	Gly	Pro	Gly	Gly	Gly	Ser	Gly	Gly	Gly
1				5				10	

&lt;210&gt; 4

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: artificially  
synthesized sequence

&lt;400&gt; 4

Gly	Gly	Pro	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly
1				5				10					15		

Ser	Gly	Gly	Gly
			20

&lt;210&gt; 5

&lt;211&gt; 30

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: artificially  
synthesized sequence

&lt;400&gt; 5

Gly Gly Pro Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly  
 1 5 10 15

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 20 25 30

<210> 6

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 6

Gly Gly Ser Gly Gly Gly Ala Ser Gly Gly  
 1 5 10

<210> 7

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 7

gggcgggatcc ggactcagaa tctccccaga cgccgag

37

<210> 8

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
 synthesized sequence

<400> 8

ccgcctcgag ctggggagga aacaggtcag catgggaac

39

<210> 9

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 9

ggcacgagcc gagatgtctc gtcctgtggc

30

<210> 10

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 10

aatttggaat tcatccaatc caaatgcggc

30

<210> 11

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 11

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

<210> 12

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 12

ggaggtggcg ggtccggagg tggttctggt ggaggttcga tccagcgtac tccaaagatt 60

<210> 13

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 13

tctggcctgg aggctagata tccactgacc tttggatggt gcttcggagg aggtggcggg 60

tcc

63

<210> 14

<211> 63

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

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tctggcctgg aggctagata cctaagggat caacagctcc tagggattgg aggtggcggg 60

tcc

63

<210> 15

<211> 81

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 15

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tctctttctg gcctggaggc t 81

<210> 16

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 16

ttgcgccgc gatgaacttt caccctaagt ttttcttact acggcgtacg ttacatgtct 60

cgatcccact t 71

<210> 12

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 17

tgcggccgcc gtacggccga gatgtctcgc tccgtggcct ta 42

<210> 18

<211> 80

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (21).. (80)

<400> 18

gcggccgccg tacggccgag atg tct cgc tcc gtg gcc tta gct gtg ctc gcg 53

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala

1 5 10

cta ctc tct ctt tct ggc ctg gag gct

80

Leu Leu Ser Leu Ser Gly Leu Glu Ala

15 20

<210> 19

<211> 20

<212> PRT

<213> Artificial Sequence

<400> 19

Met Ser Arg Ser Val Ala Leu Ala Val Leu Ala Leu Leu Ser Leu Ser

1 5 10 15

Gly Leu Glu Ala

20

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (1).. (30)

<400> 20

aga tat cca ctg acc ttt gga tgg tgc ttc  
Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe  
1 5 10

30

<210> 21

<211> 10

<212> PRT

<213> Artificial Sequence

<400> 21

Arg Tyr Pro Leu Thr Phe Gly Trp Cys Phe  
1 5 10

<210> 22

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<220>

<221> CDS

<222> (1).. (33)

<400> 22

aga tac cta agg gat caa cag ctc cta ggg att  
Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile  
1 5 10

33

<210> 23

<211> 11

<212> PRT

<213> Artificial Sequence

<400> 23

Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile



1 5 10

<210> 24

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<220>

<221> CDS

<222> (1).. (60)

<400> 24

gga ggt ggc ggg tcc gga ggt ggt tct ggt gga ggt tcg atc cag cgt	48
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ile Gln Arg	
1 5 10 15	

act cca aag att	60
Thr Pro Lys Ile	
20	

<210> 25

<211> 20

<212> PRT

<213> Artificial Sequence

<400> 25

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Ile Gln Arg	
1 5 10 15	

Thr Pro Lys Ile
20

<210> 26

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (1).. (18)

<400> 26

aag tgg gat cga gac atg taacgtacgc cgtagtaaga aaaacttagg 48  
Lys Trp Asp Arg Asp Met  
1 5

gtgaaagttc atcgcgccgc c 69

<210> 27

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 27

Lys Trp Asp Arg Asp Met  
1 5

<210> 28

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 28

tgcggccgcc gtacgccgag gatggccgctc atggcgcccc g 41

<210> 29

<211> 71

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<400> 29

ttgcggccgc gatgaacttt caccctaagt ttttcttact acggcgtacg tcacacttta 60

caagctgtga g

71

<210> 30

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially  
synthesized sequence

<220>

<221> CDS

<222> (21).. (38)

<400> 30

gcggccgcccg tacgccgagg atg gcc gtc atg gcg ccc

38

Met Ala Val Met Ala Pro

1

5

<210> 31

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 31

Met Ala Val Met Ala Pro

1

5

<210> 32

<211> 69

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (1).. (18)

<400> 32

ctc aca gct tgt aaa gtg tgacgtacgc cgtagtaaga aaaacttagg 48  
Leu Thr Ala Cys Lys Val  
1 5

gtgaaagttc atcgcggccg c 69

<210> 33

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 33

Leu Thr Ala Cys Lys Val  
1 5

<210> 34

<211> 64

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 34

tgcggccgca gtaagaaaaa cttagggtca aacgtacggc cgagatgtcg tgggccctgg 60  
aaat 64

<210> 35

<211> 56

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 35

ttgcggccgc tatcaatggt ggtgatggtg gtgagctcca cgggttaccg gattac 56

<210> 36

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 36

tgcggccgcc actccttcac tatggatctc ttg 33

<210> 37

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 37

ctacggcgta cgtcaatggt ggtgatggtg gtgagctccg gagccacaac gtcgaat 57

<210> 38

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<400> 38  
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<210> 39  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: artificially  
 synthesized sequence

<220>  
 <221> CDS  
 <222> (43).. (60)

<400> 39  
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 Met Ser Trp Ala  
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ctg gaa 60  
 Leu Glu  
 5

<210> 40  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<400> 40  
 Met Ser Trp Ala Leu Glu  
 1 5

<210> 41  
 <211> 55  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (1).. (42)

<400> 41

cgt aat ccg gta acc cgt gga gct cac cac cat cac cac cat	42
Arg Asn Pro Val Thr Arg Gly Ala His His His His His His	
1 5 10	

tgatagcggc cgc	55
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<210> 42

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 42

Arg Asn Pro Val Thr Arg Gly Ala His His His His His His	
1 5 10	

<210> 43

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized sequence

<220>

<221> CDS

<222> (41).. (58)

<400> 43

gcggccgcag taagaaaaac ttaggggtcaa agccttcact atg gat ctc ttg att	55
Met Asp Leu Leu Ile	
1 5	

cgt	58
-----	----

Arg

&lt;210&gt; 44

&lt;211&gt; 6

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 44

Met Asp Leu Leu Ile Arg  
 1 5

&lt;210&gt; 45

&lt;211&gt; 55

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: artificially  
 synthesized sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (42)

&lt;400&gt; 45

att cga cgt tgt ggc tcc gga gct cac cac cat cac cac cat 42  
 Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His  
 1 5 10

tgatagcggc cgc 55

&lt;210&gt; 46

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;400&gt; 46

Ile Arg Arg Cys Gly Ser Gly Ala His His His His His His  
 1 5 10



<210> 47  
 <211> 2960  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (165).. (2588)  
 <223>

<400> 47  
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 tatctagtga gcaggcggcc gctttcgatt tcgctttccc ctaa atg gct gag ctt 176  
 Met Ala Glu Leu  
 1  
 ctc gcc agc gca gga tca gcc tgt tcc tgg gac ttt ccg aga gcc ccg 224  
 Leu Ala Ser Ala Gly Ser Ala Cys Ser Trp Asp Phe Pro Arg Ala Pro  
 5 10 15 20  
 ccc tcg ttc cct ccc cca gcc gcc agt agg gga gga ctc ggc ggt acc 272  
 Pro Ser Phe Pro Pro Pro Ala Ala Ser Arg Gly Gly Leu Gly Gly Thr  
 25 30 35  
 cgg agc ttc agg ccc cac cgg ggc gcg gag agt ccc agg ccc ggc cgg 320  
 Arg Ser Phe Arg Pro His Arg Gly Ala Glu Ser Pro Arg Pro Gly Arg  
 40 45 50  
 gac cgg gac ggc gtc cga gtg cca atg gct agc tct agg tgt ccc gct 368  
 Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser Arg Cys Pro Ala  
 55 60 65  
 ccc cgc ggg tgc cgc tgc ctc ccc gga gct tct ctc gca tgg ctg ggg 416  
 Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu Ala Trp Leu Gly  
 70 75 80  
 aca gta ctg cta ctt ctc gcc gac tgg gtg ctg ctc cgg acc gcg ctg 464  
 Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu Arg Thr Ala Leu  
 85 90 95 100  
 ccc cgc ata ttc tcc ctg ctg gtg ccc acc gcg ctg cca ctg ctc cgg 512

Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu Pro Leu Leu Arg	
105 110 115	
gtc tgg gcg gtg ggc ctg agc cgc tgg gcc gtg ctc tgg ctg ggg gcc	560
Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu Trp Leu Gly Ala	
120 125 130	
tgc ggg gtc ctc agg gca acg gtt ggc tcc aag agc gaa aac gca ggt	608
Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser Glu Asn Ala Gly	
135 140 145	
gcc cag ggc tgg ctg gct gct ttg aag cca tta gct gcg gca ctg ggc	656
Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala Ala Ala Leu Gly	
150 155 160	
ttg gcc ctg ccg gga ctt gcc ttg ttc cga gag ctg atc tca tgg gga	704
Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu Ile Ser Trp Gly	
165 170 175 180	
gcc ccc ggg tcc gcg gat agc acc agg cta ctg cac tgg gga agt cac	752
Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His Trp Gly Ser His	
185 190 195	
cct acc gcc ttc gtt gtc agt tat gca gcg gca ctg ccc gca gca gcc	800
Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu Pro Ala Ala Ala	
200 205 210	
ctg tgg cac aaa ctc ggg agc ctc tgg gtg ccc ggc ggt cag ggc ggc	848
Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly Gly Gln Gly Gly	
215 220 225	
tct gga aac cct gtg cgt cgg ctt cta ggc tgc ctg ggc tcg gag acg	896
Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu Gly Ser Glu Thr	
230 235 240	
cgc cgc ctc tcg ctg ttc ctg gtc ctg gtg gtc ctc tcc tct ctt ggg	944
Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu Ser Ser Leu Gly	
245 250 255 260	
gag atg gcc att cca ttc ttt acg ggc cgc ctc act gac tgg att cta	992
Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr Asp Trp Ile Leu	
265 270 275	
caa gat ggc tca gcc gat acc ttc act cga aac tta act ctc atg tcc	1040

Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu Thr Leu Met Ser	
280 285 290	
att ctc acc ata gcc agt gca gtg ctg gag ttc gtg ggt gac ggg atc	1088
Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val Gly Asp Gly Ile	
295 300 305	
tat aac aac acc atg ggc cac gtg cac agc cac ttg cag gga gag gtg	1136
Tyr Asn Asn Thr Met Gly His Val His Ser His Leu Gln Gly Glu Val	
310 315 320	
ttt ggg gct gtc ctg cgc cag gag acg gag ttt ttc caa cag aac cag	1184
Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe Gln Gln Asn Gln	
325 330 335 340	
aca ggt aac atc atg tct cgg gta aca gag gac acg tcc acc ctg agt	1232
Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr Ser Thr Leu Ser	
345 350 355	
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Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp Tyr Leu Val Arg	
360 365 370	
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Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser Val Ser Leu Thr	
375 380 385	
atg gtc acc ctg atc acc ctg cct ctg ctt ttc ctt ctg ccc aag aag	1376
Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu Leu Pro Lys Lys	
390 395 400	
gtg gga aaa tgg tac cag ttg ctg gaa gtg cag gtg cgg gaa tct ctg	1424
Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val Arg Glu Ser Leu	
405 410 415 420	
gca aag tcc agc cag gtg gcc att gag gct ctg tcg gcc atg cct aca	1472
Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser Ala Met Pro Thr	
425 430 435	
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Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln Lys Phe Arg Glu	
440 445 450	
aag ctg caa gaa ata aag aca ctc aac cag aag gag gct gtg gcc tat	1568

Lys	Leu	Gln	Glu	Ile	Lys	Thr	Leu	Asn	Gln	Lys	Glu	Ala	Val	Ala	Tyr		
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Ala	Val	Asn	Ser	Trp	Thr	Thr	Ser	Ile	Ser	Gly	Met	Leu	Leu	Lys	Val		
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Ser	Gly	Asn	Leu	Val	Thr	Phe	Val	Leu	Tyr	Gln	Met	Gln	Phe	Thr	Gln		
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Gly	Ser	Ser	Glu	Lys	Ile	Phe	Glu	Tyr	Leu	Asp	Arg	Thr	Pro	Arg	Cys		
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Pro	Pro	Ser	Gly	Leu	Leu	Thr	Pro	Leu	His	Leu	Glu	Gly	Leu	Val	Gln		
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Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Ala	Leu	Leu	Gln		
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Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	Gln	Leu	Leu	Leu	Asp	Gly	Lys	Pro		
			615				620					625					
ctt	ccc	caa	tat	gag	cac	cgc	tac	ctg	cac	agg	cag	gtg	gct	gca	gtg	2096	

Leu Pro Gln Tyr Glu His Arg Tyr Leu His Arg Gln Val Ala Ala Val	
630 635 640	
gga caa gag cca cag gta ttt gga aga agt ctt caa gaa aat att gcc	2144
Gly Gln Glu Pro Gln Val Phe Gly Arg Ser Leu Gln Glu Asn Ile Ala	
645 650 655 660	
tat ggc ctg acc cag aag cca act atg gag gaa atc aca gct gct gca	2192
Tyr Gly Leu Thr Gln Lys Pro Thr Met Glu Glu Ile Thr Ala Ala Ala	
665 670 675	
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Val Lys Ser Gly Ala His Ser Phe Ile Ser Gly Leu Pro Gln Gly Tyr	
680 685 690	
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Asp Thr Glu Val Asp Glu Ala Gly Ser Gln Leu Ser Gly Gly Gln Arg	
695 700 705	
cag gca gtg gcg ttg gcc cga gca ttg atc cgg aaa ccg tgt gta ctt	2336
Gln Ala Val Ala Leu Ala Arg Ala Leu Ile Arg Lys Pro Cys Val Leu	
710 715 720	
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Ile Leu Asp Asp Ala Thr Ser Ala Leu Asp Ala Asn Ser Gln Leu Gln	
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Val Glu Gln Leu Leu Tyr Glu Ser Pro Glu Arg Tyr Ser Arg Ser Val	
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Leu Leu Ile Thr Gln His Leu Ser Leu Val Glu Gln Ala Asp His Ile	
760 765 770	
ctc ttt ctg gaa gga ggc gct atc cgg gag ggg gga acc cac cag cag	2528
Leu Phe Leu Glu Gly Gly Ala Ile Arg Glu Gly Gly Thr His Gln Gln	
775 780 785	
ctc atg gag aaa aag ggg tgc tac tgg gcc atg gtg cag gct cct gca	2576
Leu Met Glu Lys Lys Gly Cys Tyr Trp Ala Met Val Gln Ala Pro Ala	
790 795 800	
gat gct cca gaa tgaaagcctt ctgagacctg cgcaactccat ctccctccct	2628

Asp Ala Pro Glu

805

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cttcctggag tacaacaca ggatttgtaa ttccttactg taacggagtt tagagccagg 2808
gctgatgctt tgggtgtggc agcactctga aactgagaaa tggtcagaat gtacggaaag 2868
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tcttgatatt tataataaaa ttggtgtttt gt 2960

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&lt;210&gt; 48

&lt;211&gt; 808

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 48

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Pro Arg Ala Pro Pro Ser Phe Pro Pro Pro Ala Ala Ser Arg Gly Gly
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Leu Gly Gly Thr Arg Ser Phe Arg Pro His Arg Gly Ala Glu Ser Pro
          35          40          45

Arg Pro Gly Arg Asp Arg Asp Gly Val Arg Val Pro Met Ala Ser Ser
          50          55          60

Arg Cys Pro Ala Pro Arg Gly Cys Arg Cys Leu Pro Gly Ala Ser Leu
65          70          75          80

Ala Trp Leu Gly Thr Val Leu Leu Leu Leu Ala Asp Trp Val Leu Leu
          85          90          95

Arg Thr Ala Leu Pro Arg Ile Phe Ser Leu Leu Val Pro Thr Ala Leu
          100          105          110

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Pro Leu Leu Arg Val Trp Ala Val Gly Leu Ser Arg Trp Ala Val Leu  
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Trp Leu Gly Ala Cys Gly Val Leu Arg Ala Thr Val Gly Ser Lys Ser  
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Glu Asn Ala Gly Ala Gln Gly Trp Leu Ala Ala Leu Lys Pro Leu Ala  
 145 150 155 160

Ala Ala Leu Gly Leu Ala Leu Pro Gly Leu Ala Leu Phe Arg Glu Leu  
 165 170 175

Ile Ser Trp Gly Ala Pro Gly Ser Ala Asp Ser Thr Arg Leu Leu His  
 180 185 190

Trp Gly Ser His Pro Thr Ala Phe Val Val Ser Tyr Ala Ala Ala Leu  
 195 200 205

Pro Ala Ala Ala Leu Trp His Lys Leu Gly Ser Leu Trp Val Pro Gly  
 210 215 220

Gly Gln Gly Gly Ser Gly Asn Pro Val Arg Arg Leu Leu Gly Cys Leu  
 225 230 235 240

Gly Ser Glu Thr Arg Arg Leu Ser Leu Phe Leu Val Leu Val Val Leu  
 245 250 255

Ser Ser Leu Gly Glu Met Ala Ile Pro Phe Phe Thr Gly Arg Leu Thr  
 260 265 270

Asp Trp Ile Leu Gln Asp Gly Ser Ala Asp Thr Phe Thr Arg Asn Leu  
 275 280 285

Thr Leu Met Ser Ile Leu Thr Ile Ala Ser Ala Val Leu Glu Phe Val  
 290 295 300

Gly Asp Gly Ile Tyr Asn Asn Thr Met Gly His Val His Ser His Leu  
 305 310 315 320

Gln Gly Glu Val Phe Gly Ala Val Leu Arg Gln Glu Thr Glu Phe Phe  
 325 330 335

Gln Gln Asn Gln Thr Gly Asn Ile Met Ser Arg Val Thr Glu Asp Thr  
 340 345 350

Ser Thr Leu Ser Asp Ser Leu Ser Glu Asn Leu Ser Leu Phe Leu Trp  
 355 360 365

Tyr Leu Val Arg Gly Leu Cys Leu Leu Gly Ile Met Leu Trp Gly Ser  
 370 375 380

Val Ser Leu Thr Met Val Thr Leu Ile Thr Leu Pro Leu Leu Phe Leu  
 385 390 395 400

Leu Pro Lys Lys Val Gly Lys Trp Tyr Gln Leu Leu Glu Val Gln Val  
 405 410 415

Arg Glu Ser Leu Ala Lys Ser Ser Gln Val Ala Ile Glu Ala Leu Ser  
 420 425 430

Ala Met Pro Thr Val Arg Ser Phe Ala Asn Glu Glu Gly Glu Ala Gln  
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Lys Phe Arg Glu Lys Leu Gln Glu Ile Lys Thr Leu Asn Gln Lys Glu  
 450 455 460

Ala Val Ala Tyr Ala Val Asn Ser Trp Thr Thr Ser Ile Ser Gly Met  
 465 470 475 480

Leu Leu Lys Val Gly Ile Leu Tyr Ile Gly Gly Gln Leu Val Thr Ser  
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Gly Ala Val Ser Ser Gly Asn Leu Val Thr Phe Val Leu Tyr Gln Met  
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Gln Phe Thr Gln Ala Val Glu Val Leu Leu Ser Ile Tyr Pro Arg Val  
 515 520 525

Gln Lys Ala Val Gly Ser Ser Glu Lys Ile Phe Glu Tyr Leu Asp Arg  
 530 535 540

Thr Pro Arg Cys Pro Pro Ser Gly Leu Leu Thr Pro Leu His Leu Glu  
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Gly Leu Val Gln Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro  
 565 570 575

Asp Val Leu Val Leu Gln Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu



580				585				590							
Val	Thr	Ala	Leu	Val	Gly	Pro	Asn	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala
		595					600					605			
Ala	Leu	Leu	Gln	Asn	Leu	Tyr	Gln	Pro	Thr	Gly	Gly	Gln	Leu	Leu	Leu
	610					615					620				
Asp	Gly	Lys	Pro	Leu	Pro	Gln	Tyr	Glu	His	Arg	Tyr	Leu	His	Arg	Gln
625					630					635					640
Val	Ala	Ala	Val	Gly	Gln	Glu	Pro	Gln	Val	Phe	Gly	Arg	Ser	Leu	Gln
				645					650					655	
Glu	Asn	Ile	Ala	Tyr	Gly	Leu	Thr	Gln	Lys	Pro	Thr	Met	Glu	Glu	Ile
			660					665					670		
Thr	Ala	Ala	Ala	Val	Lys	Ser	Gly	Ala	His	Ser	Phe	Ile	Ser	Gly	Leu
			675				680					685			
Pro	Gln	Gly	Tyr	Asp	Thr	Glu	Val	Asp	Glu	Ala	Gly	Ser	Gln	Leu	Ser
	690					695					700				
Gly	Gly	Gln	Arg	Gln	Ala	Val	Ala	Leu	Ala	Arg	Ala	Leu	Ile	Arg	Lys
705					710					715					720
Pro	Cys	Val	Leu	Ile	Leu	Asp	Asp	Ala	Thr	Ser	Ala	Leu	Asp	Ala	Asn
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Ser	Gln	Leu	Gln	Val	Glu	Gln	Leu	Leu	Tyr	Glu	Ser	Pro	Glu	Arg	Tyr
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Ser	Arg	Ser	Val	Leu	Leu	Ile	Thr	Gln	His	Leu	Ser	Leu	Val	Glu	Gln
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Ala	Asp	His	Ile	Leu	Phe	Leu	Glu	Gly	Gly	Ala	Ile	Arg	Glu	Gly	Gly
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Thr	His	Gln	Gln	Leu	Met	Glu	Lys	Lys	Gly	Cys	Tyr	Trp	Ala	Met	Val
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Gln	Ala	Pro	Ala	Asp	Ala	Pro	Glu								
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 Met Arg Leu Pro Asp Leu  
 1 5  
 aga ccc tgg acc tcc ctg ctg ctg gtg gac gcg gct tta ctg tgg ctg 162  
 Arg Pro Trp Thr Ser Leu Leu Leu Val Asp Ala Ala Leu Leu Trp Leu  
 10 15 20  
 ctt cag ggc cct ctg ggg act ttg ctt cct caa ggg ctg cca gga cta 210  
 Leu Gln Gly Pro Leu Gly Thr Leu Leu Pro Gln Gly Leu Pro Gly Leu  
 25 30 35  
 tgg ctg gag ggg acc ctg cgg ctg gga ggg ctg tgg ggg ctg cta aag 258  
 Trp Leu Glu Gly Thr Leu Arg Leu Gly Gly Leu Trp Gly Leu Leu Lys  
 40 45 50  
 cta aga ggg ctg ctg gga ttt gtg ggg aca ctg ctg ctc ccg ctc tgt 306  
 Leu Arg Gly Leu Leu Gly Phe Val Gly Thr Leu Leu Leu Pro Leu Cys  
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 ctg gcc acc ccc ctg act gtc tcc ctg aga gcc ctg gtc gcg ggg gcc 354  
 Leu Ala Thr Pro Leu Thr Val Ser Leu Arg Ala Leu Val Ala Gly Ala  
 75 80 85  
 tca cgt gct ccc cca gcc aga gtc gct tca gcc cct tgg agc tgg ctg 402  
 Ser Arg Ala Pro Pro Ala Arg Val Ala Ser Ala Pro Trp Ser Trp Leu  
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 ctg gtg ggg tac ggg gct gcg ggg ctc agc tgg tca ctg tgg gct gtt 450  
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105	110	115	
ctg agc cct cct gga gcc cag gag aag gag cag gac cag gtg aac aac			498
Leu Ser Pro Pro Gly Ala Gln Glu Lys Glu Gln Asp Gln Val Asn Asn			
120	125	130	
aaa gtc ttg atg tgg agg ctg ctg aag ctc tcc agg ccg gac ctg cct			546
Lys Val Leu Met Trp Arg Leu Leu Lys Leu Ser Arg Pro Asp Leu Pro			
135	140	145	150
ctc ctc gtt gcc gcc ttc ttc ttc ctt gtc ctt gct gtt ttg ggt gag			594
Leu Leu Val Ala Ala Phe Phe Phe Leu Val Leu Ala Val Leu Gly Glu			
	155	160	165
aca tta atc cct cac tat tct ggt cgt gtg att gac atc ctg gga ggt			642
Thr Leu Ile Pro His Tyr Ser Gly Arg Val Ile Asp Ile Leu Gly Gly			
	170	175	180
gat ttt gac ccc cat gcc ttt gcc agt gcc atc ttc ttc atg tgc ctc			690
Asp Phe Asp Pro His Ala Phe Ala Ser Ala Ile Phe Phe Met Cys Leu			
	185	190	195
ttc tcc ttt ggc agc tca ctg tct gca ggc tgc cga gga ggc tgc ttc			738
Phe Ser Phe Gly Ser Ser Leu Ser Ala Gly Cys Arg Gly Gly Cys Phe			
200	205	210	
acc tac acc atg tct cga atc aac ttg cgg atc cgg gag cag ctt ttc			786
Thr Tyr Thr Met Ser Arg Ile Asn Leu Arg Ile Arg Glu Gln Leu Phe			
215	220	225	230
tcc tcc ctg ctg cgc cag gac ctc ggt ttc ttc cag gag act aag aca			834
Ser Ser Leu Leu Arg Gln Asp Leu Gly Phe Phe Gln Glu Thr Lys Thr			
	235	240	245
ggg gag ctg aac tca cgg ctg agc tcg gat acc acc ctg atg agt aac			882
Gly Glu Leu Asn Ser Arg Leu Ser Ser Asp Thr Thr Leu Met Ser Asn			
	250	255	260
tgg ctt cct tta aat gcc aat gtg ctc ttg cga agc ctg gtg aaa gtg			930
Trp Leu Pro Leu Asn Ala Asn Val Leu Leu Arg Ser Leu Val Lys Val			
265	270	275	
gtg ggg ctg tat ggc ttc atg ctc agc ata tcg cct cga ctc acc ctc			978
Val Gly Leu Tyr Gly Phe Met Leu Ser Ile Ser Pro Arg Leu Thr Leu			

280	285	290	
ctt tct ctg ctg cac atg ccc ttc aca ata gca gcg gag aag gtg tac			1026
Leu Ser Leu Leu His Met Pro Phe Thr Ile Ala Ala Glu Lys Val Tyr			
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aac acc cgc cat cag gaa gtg ctt cgg gag atc cag gat gca gtg gcc			1074
Asn Thr Arg His Gln Glu Val Leu Arg Glu Ile Gln Asp Ala Val Ala			
	315	320	325
agg gcg ggg cag gtg gtg cgg gaa gcc gtt gga ggg ctg cag acc gtt			1122
Arg Ala Gly Gln Val Val Arg Glu Ala Val Gly Gly Leu Gln Thr Val			
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cgc agt ttt ggg gcc gag gag cat gaa gtc tgt cgc tat aaa gag gcc			1170
Arg Ser Phe Gly Ala Glu Glu His Glu Val Cys Arg Tyr Lys Glu Ala			
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ctt gaa caa tgt cgg cag ctg tat tgg cgg aga gac ctg gaa cgc gcc			1218
Leu Glu Gln Cys Arg Gln Leu Tyr Trp Arg Arg Asp Leu Glu Arg Ala			
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ttg tac ctg ctc ata agg agg gtg ctg cac ttg ggg gtg cag atg ctg			1266
Leu Tyr Leu Leu Ile Arg Arg Val Leu His Leu Gly Val Gln Met Leu			
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atg ctg agc tgt ggg ctg cag cag atg cag gat ggg gag ctc acc cag			1314
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ggc agc ctg ctt tcc ttt atg atc tac cag gag agc gtg ggg agc tat			1362
Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln Glu Ser Val Gly Ser Tyr			
	410	415	420
gtg cag acc ctg gta tac ata tat ggg gat atg ctc agc aac gtg gga			1410
Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp Met Leu Ser Asn Val Gly			
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gct gca gag aag gtt ttc tcc tac atg gac cga cag cca aat ctg cct			1458
Ala Ala Glu Lys Val Phe Ser Tyr Met Asp Arg Gln Pro Asn Leu Pro			
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tca cct ggc acg ctt gcc ccc acc act ctg cag ggg gtt gtg aaa ttc			1506
Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu Gln Gly Val Val Lys Phe			

455	460	465	470	
caa gac gtc tcc ttt gca tat ccc aat cgc cct gac agg cct gtg ctc				1554
Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg Pro Asp Arg Pro Val Leu				
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aag ggg ctg acg ttt acc cta cgt cct ggt gag gtg acg gcg ctg gtg				1602
Lys Gly Leu Thr Phe Thr Leu Arg Pro Gly Glu Val Thr Ala Leu Val				
	490	495	500	
gga ccc aat ggg tct ggg aag agc aca gtg gct gcc ctg ctg cag aat				1650
Gly Pro Asn Gly Ser Gly Lys Ser Thr Val Ala Ala Leu Leu Gln Asn				
	505	510	515	
ctg tac cag ccc aca ggg gga cag gtg ctg ctg gat gaa aag ccc atc				1698
Leu Tyr Gln Pro Thr Gly Gly Gln Val Leu Leu Asp Glu Lys Pro Ile				
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tca cag tat gaa cac tgc tac ctg cac agc cag gtg gtt tca gtt ggg				1746
Ser Gln Tyr Glu His Cys Tyr Leu His Ser Gln Val Val Ser Val Gly				
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cag gag cct gtg ctg ttc tcc ggt tct gtg agg aac aac att gct tat				1794
Gln Glu Pro Val Leu Phe Ser Gly Ser Val Arg Asn Asn Ile Ala Tyr				
	555	560	565	
ggg ctg cag agc tgc gaa gat gat aag gtg atg gcg gct gcc cag gct				1842
Gly Leu Gln Ser Cys Glu Asp Asp Lys Val Met Ala Ala Ala Gln Ala				
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gcc cac gca gat gac ttc atc cag gaa atg gag cat gga ata tac aca				1890
Ala His Ala Asp Asp Phe Ile Gln Glu Met Glu His Gly Ile Tyr Thr				
	585	590	595	
gat gta ggg gag aag gga agc cag ctg gct gcg gga cag aaa caa cgt				1938
Asp Val Gly Glu Lys Gly Ser Gln Leu Ala Ala Gly Gln Lys Gln Arg				
	600	605	610	
ctg gcc att gcc cgg gcc ctt gta cga gac ccg cgg gtc ctc atc ctg				1986
Leu Ala Ile Ala Arg Ala Leu Val Arg Asp Pro Arg Val Leu Ile Leu				
	615	620	625	630
gat gag gct act agt gcc cta gat gtg cag tgc gag cag gcc ctg cag				2034
Asp Glu Ala Thr Ser Ala Leu Asp Val Gln Cys Glu Gln Ala Leu Gln				

635	640	645	
gac tgg aat tcc cgt ggg gat cgc aca gtg ctg gtg att gct cac agg			2082
Asp Trp Asn Ser Arg Gly Asp Arg Thr Val Leu Val Ile Ala His Arg			
650	655	660	
ctg cag gca gtt cag cgc gcc cac cag atc ctg gtg ctc cag gag ggc			2130
Leu Gln Ala Val Gln Arg Ala His Gln Ile Leu Val Leu Gln Glu Gly			
665	670	675	
aag ctg cag aag ctt gcc cag ctc cag gag gga cag gac ctc tat tcc			2178
Lys Leu Gln Lys Leu Ala Gln Leu Gln Glu Gly Gln Asp Leu Tyr Ser			
680	685	690	
cgc ctg gtt cag cag cgg ctg atg gac tgaggcccca gggatactgg			2225
Arg Leu Val Gln Gln Arg Leu Met Asp			
695	700		
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cttcctggag ataaccatag ttgctatttt gctgcctgtc ccatcagtcg tttatctggt			2645
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 tccctttccc accttttttg accttccact agaccatgag cacctgggcg gaaagccata 3665  
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Ala	Ala	Leu	Leu	Trp	Leu	Leu	Gln	Gly	Pro	Leu	Gly	Thr	Leu	Leu	Pro
		20					25					30			
Gln	Gly	Leu	Pro	Gly	Leu	Trp	Leu	Glu	Gly	Thr	Leu	Arg	Leu	Gly	Gly
		35				40					45				
Leu	Trp	Gly	Leu	Leu	Lys	Leu	Arg	Gly	Leu	Leu	Gly	Phe	Val	Gly	Thr
	50					55					60				

Leu Leu Leu Pro Leu Cys Leu Ala Thr Pro Leu Thr Val Ser Leu Arg  
 65 70 75 80

Ala Leu Val Ala Gly Ala Ser Arg Ala Pro Pro Ala Arg Val Ala Ser  
 85 90 95

Ala Pro Trp Ser Trp Leu Leu Val Gly Tyr Gly Ala Ala Gly Leu Ser  
 100 105 110

Trp Ser Leu Trp Ala Val Leu Ser Pro Pro Gly Ala Gln Glu Lys Glu  
 115 120 125

Gln Asp Gln Val Asn Asn Lys Val Leu Met Trp Arg Leu Leu Lys Leu  
 130 135 140

Ser Arg Pro Asp Leu Pro Leu Leu Val Ala Ala Phe Phe Phe Leu Val  
 145 150 155 160

Leu Ala Val Leu Gly Glu Thr Leu Ile Pro His Tyr Ser Gly Arg Val  
 165 170 175

Ile Asp Ile Leu Gly Gly Asp Phe Asp Pro His Ala Phe Ala Ser Ala  
 180 185 190

Ile Phe Phe Met Cys Leu Phe Ser Phe Gly Ser Ser Leu Ser Ala Gly  
 195 200 205

Cys Arg Gly Gly Cys Phe Thr Tyr Thr Met Ser Arg Ile Asn Leu Arg  
 210 215 220

Ile Arg Glu Gln Leu Phe Ser Ser Leu Leu Arg Gln Asp Leu Gly Phe  
 225 230 235 240

Phe Gln Glu Thr Lys Thr Gly Glu Leu Asn Ser Arg Leu Ser Ser Asp  
 245 250 255

Thr Thr Leu Met Ser Asn Trp Leu Pro Leu Asn Ala Asn Val Leu Leu  
 260 265 270

Arg Ser Leu Val Lys Val Val Gly Leu Tyr Gly Phe Met Leu Ser Ile  
 275 280 285

Ser Pro Arg Leu Thr Leu Leu Ser Leu Leu His Met Pro Phe Thr Ile  
 290 295 300



Ala Ala Glu Lys Val Tyr Asn Thr Arg His Gln Glu Val Leu Arg Glu  
305 310 315 320

Ile Gln Asp Ala Val Ala Arg Ala Gly Gln Val Val Arg Glu Ala Val  
325 330 335

Gly Gly Leu Gln Thr Val Arg Ser Phe Gly Ala Glu Glu His Glu Val  
340 345 350

Cys Arg Tyr Lys Glu Ala Leu Glu Gln Cys Arg Gln Leu Tyr Trp Arg  
355 360 365

Arg Asp Leu Glu Arg Ala Leu Tyr Leu Leu Ile Arg Arg Val Leu His  
370 375 380

Leu Gly Val Gln Met Leu Met Leu Ser Cys Gly Leu Gln Gln Met Gln  
385 390 395 400

Asp Gly Glu Leu Thr Gln Gly Ser Leu Leu Ser Phe Met Ile Tyr Gln  
405 410 415

Glu Ser Val Gly Ser Tyr Val Gln Thr Leu Val Tyr Ile Tyr Gly Asp  
420 425 430

Met Leu Ser Asn Val Gly Ala Ala Glu Lys Val Phe Ser Tyr Met Asp  
435 440 445

Arg Gln Pro Asn Leu Pro Ser Pro Gly Thr Leu Ala Pro Thr Thr Leu  
450 455 460

Gln Gly Val Val Lys Phe Gln Asp Val Ser Phe Ala Tyr Pro Asn Arg  
465 470 475 480

Pro Asp Arg Pro Val Leu Lys Gly Leu Thr Phe Thr Leu Arg Pro Gly  
485 490 495

Glu Val Thr Ala Leu Val Gly Pro Asn Gly Ser Gly Lys Ser Thr Val  
500 505 510

Ala Ala Leu Leu Gln Asn Leu Tyr Gln Pro Thr Gly Gly Gln Val Leu  
515 520 525

Leu Asp Glu Lys Pro Ile Ser Gln Tyr Glu His Cys Tyr Leu His Ser

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Gln Val Val Ser Val Gly Gln Glu Pro Val Leu Phe Ser Gly Ser Val				
545		550		555
				560
Arg Asn Asn Ile Ala Tyr Gly Leu Gln Ser Cys Glu Asp Asp Lys Val				
	565		570	575
Met Ala Ala Ala Gln Ala Ala His Ala Asp Asp Phe Ile Gln Glu Met				
	580		585	590
Glu His Gly Ile Tyr Thr Asp Val Gly Glu Lys Gly Ser Gln Leu Ala				
	595		600	605
Ala Gly Gln Lys Gln Arg Leu Ala Ile Ala Arg Ala Leu Val Arg Asp				
	610		615	620
Pro Arg Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Val Gln				
	625		630	635
				640
Cys Glu Gln Ala Leu Gln Asp Trp Asn Ser Arg Gly Asp Arg Thr Val				
	645		650	655
Leu Val Ile Ala His Arg Leu Gln Ala Val Gln Arg Ala His Gln Ile				
	660		665	670
Leu Val Leu Gln Glu Gly Lys Leu Gln Lys Leu Ala Gln Leu Gln Glu				
	675		680	685
Gly Gln Asp Leu Tyr Ser Arg Leu Val Gln Gln Arg Leu Met Asp				
	690		695	700

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 Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg  
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 Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu  
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 Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn  
 50 55 60

gca tcc ttg ggt gtg gca cat cga aga acc ggc ggg acc gtg acc gac 240  
 Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp  
 65 70 75 80

agt ccc cgt aat ccg gta acc cgt 264  
 Ser Pro Arg Asn Pro Val Thr Arg  
 85

<210> 52

<211> 88

<212> PRT

<213> human herpesvirus 1

<400> 52

Met Ser Trp Ala Leu Glu Met Ala Asp Thr Phe Leu Asp Thr Met Arg  
 1 5 10 15

Val Gly Pro Arg Thr Tyr Ala Asp Val Arg Asp Glu Ile Asn Lys Arg  
 20 25 30

Gly Arg Glu Asp Arg Glu Ala Ala Arg Thr Ala Val His Asp Pro Glu  
 35 40 45

Arg Pro Leu Leu Arg Ser Pro Gly Leu Leu Pro Glu Ile Ala Pro Asn  
 50 55 60

Ala Ser Leu Gly Val Ala His Arg Arg Thr Gly Gly Thr Val Thr Asp  
65 70 75 80

Ser Pro Arg Asn Pro Val Thr Arg  
85

<210> 53  
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<220>  
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<222> (1).. (549)  
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<400> 53  
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Met Asp Leu Leu Ile Arg Leu Gly Phe Leu Leu Met Cys Ala Leu Pro  
1 5 10 15  
acc ccc ggt gag cgg tct tcg cgt gac ccg aaa acc ctt ctc tct ctg 96  
Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu  
20 25 30  
tct ccg cga caa caa gct tgt gtt ccg aga acg aag tcg cac aga ccc 144  
Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro  
35 40 45  
gtt tgt tac aac gat aca ggg gac tgc aca gat gca gat gat agc tgg 192  
Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp  
50 55 60  
aaa cag ctg ggt gag gac ttt gcg cac caa tgc ttg cag gcg gcg aaa 240  
Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys  
65 70 75 80  
aag agg cct aaa acg cac aaa tcc cgt ccg aac gat agg aac ctt gag 288  
Lys Arg Pro Lys Thr His Lys Ser Arg Pro Asn Asp Arg Asn Leu Glu  
85 90 95  
ggg agg ctg acc tgt caa cga gtc cgt cgg cta ctg ccc tgt gat ttg 336  
Gly Arg Leu Thr Cys Gln Arg Val Arg Arg Leu Leu Pro Cys Asp Leu

100	105	110	
gat att cat cct agc cac cgg ttg tta acg ctt atg aat aac tgc gtc			384
Asp Ile His Pro Ser His Arg Leu Leu Thr Leu Met Asn Asn Cys Val			
115	120	125	
tgt gac ggg gcc gtt tgg aac gcg ttt cgc ttg ata gaa cga cac gga			432
Cys Asp Gly Ala Val Trp Asn Ala Phe Arg Leu Ile Glu Arg His Gly			
130	135	140	
ttc ttc gct gtg act ttg tat tta tgt tgc ggg att act ctg ctg gtt			480
Phe Phe Ala Val Thr Leu Tyr Leu Cys Cys Gly Ile Thr Leu Leu Val			
145	150	155	160
gtt att cta gca ttg ctg tgc agc ata aca tac gaa tcg act gga cgt			528
Val Ile Leu Ala Leu Leu Cys Ser Ile Thr Tyr Glu Ser Thr Gly Arg			
165	170	175	
ggg att cga cgt tgt ggc tcc			549
Gly Ile Arg Arg Cys Gly Ser			
180			

<210> 54  
 <211> 183  
 <212> PRT  
 <213> Human cytomegalovirus

<400> 54

Met Asp Leu Leu Ile Arg Leu Gly Phe Leu Leu Met Cys Ala Leu Pro			
1	5	10	15
Thr Pro Gly Glu Arg Ser Ser Arg Asp Pro Lys Thr Leu Leu Ser Leu			
20	25	30	
Ser Pro Arg Gln Gln Ala Cys Val Pro Arg Thr Lys Ser His Arg Pro			
35	40	45	
Val Cys Tyr Asn Asp Thr Gly Asp Cys Thr Asp Ala Asp Asp Ser Trp			
50	55	60	
Lys Gln Leu Gly Glu Asp Phe Ala His Gln Cys Leu Gln Ala Ala Lys			
65	70	75	80

Lys Arg Pro Lys Thr His Lys Ser Arg Pro Asn Asp Arg Asn Leu Glu  
                     85                    90                    95

Gly Arg Leu Thr Cys Gln Arg Val Arg Arg Leu Leu Pro Cys Asp Leu  
                     100                    105                    110

Asp Ile His Pro Ser His Arg Leu Leu Thr Leu Met Asn Asn Cys Val  
                     115                    120                    125

Cys Asp Gly Ala Val Trp Asn Ala Phe Arg Leu Ile Glu Arg His Gly  
                     130                    135                    140

Phe Phe Ala Val Thr Leu Tyr Leu Cys Cys Gly Ile Thr Leu Leu Val  
                     145                    150                    155                    160

Val Ile Leu Ala Leu Leu Cys Ser Ile Thr Tyr Glu Ser Thr Gly Arg  
                     165                    170                    175

Gly Ile Arg Arg Cys Gly Ser  
                     180